

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: November 28, 2001, 19:50:29 : Search time 10.4 seconds

(without alignments)  
494.070 Million cell updat es/sec

Title: US-09-516-052-2\_COPY\_28\_177  
Perfect score: 864

Sequence: 1 REUDGYMDIANYIRIMFKTL.....YGYGLDSDMWNGGRYYUN 150

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_39.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	364	45	179	1	CHFA_MAIZE
2	324	40	179	1	CHFA_MAIZE
3	322	40	179	1	CHFA_MAIZE
4	322	40	179	1	CHFA_MAIZE
5	322	40	179	1	CHFA_MAIZE
6	322	40	179	1	CHFA_MAIZE
7	279	34	179	1	CHFA_MAIZE
8	279	34	179	1	CHFA_MAIZE
9	224	27	179	1	CHFA_MAIZE
10	151	20	179	1	CHFA_MAIZE
11	158	19	179	1	CHFA_MAIZE
12	94	11	179	1	CHFA_MAIZE
13	94	11	179	1	CHFA_MAIZE
14	92	11	179	1	CHFA_MAIZE
15	89	11	179	1	CHFA_MAIZE
16	88	10	179	1	CHFA_MAIZE
17	88	10	179	1	CHFA_MAIZE
18	87	10	179	1	CHFA_MAIZE
19	86	10	179	1	CHFA_MAIZE
20	84	10	179	1	CHFA_MAIZE
21	83	10	179	1	CHFA_MAIZE
22	83	10	179	1	CHFA_MAIZE
23	82	10	179	1	CHFA_MAIZE
24	82	10	179	1	CHFA_MAIZE
25	81	10	179	1	CHFA_MAIZE
26	79	9	179	1	CHFA_MAIZE
27	79	9	179	1	CHFA_MAIZE
28	78	9	179	1	CHFA_MAIZE
29	78	9	179	1	CHFA_MAIZE
30	76	9	179	1	CHFA_MAIZE
31	75	9	179	1	CHFA_MAIZE
32	75	9	179	1	CHFA_MAIZE
33	75	9	179	1	CHFA_MAIZE

## ALIGNMENTS

RESULT	ID	CHFA_MAIZE	STANDARD	PRT	179 AA
AC	P25209	CHFA_MAIZE	STANDARD	PRT	179 AA
DT	01-MAY-1992	(Rel. 22, Created)			
DT	01-MAY-1992	(Rel. 22, Last sequence update)			
DT	01-OCT-1996	(Rel. 34, Last annotation update)			
DE	CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CHFA-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CCAAT-BOX DNA BINDING PROTEIN SUBUNIT B).				
GN	MY2.				
OS	Zea mays (Maize).				
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACO clade: Panicoideae: Andropogoneae: Zea.				
OX	NCBI_TaxID=4577.				
RN	11				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92195809; PubMed=1549471.				
RA	Li X.-Y., Maniatis P., Beatty van Huijsduijnen R., Andre J., Benoist C., Mathis D., "Evolutionary variation of the CCAAT-binding transcription factor NF-Y."				
RT	NF-Y."				
RL	Nucleic Acids Res. 20:1087-1091(1992).				
CC	FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY RECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS. FOR EXAMPLE IN TYPE I COLLAGEN, ALBUMIN AND BETA-ACTIN GENES.				
CC	SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A AND B, THAT ARE BOTH NEEDED FOR DNA BINDING.				
CC	SUBCELLULAR LOCATION: NUCLEAR.				
CC	DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS: THE WEAKLY CONSERVED N-TERMINAL, THE RICHLY CONSERVED B-DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU-RICH C-DOMAIN.				
CC	-1- SIMILARITY: BELONGS TO THE CHFA-A SUBUNIT FAMILY.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL establishment - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, altered by, and for commercial or other purposes without the express approval of the EMBL.				
CC	or send an email to license@sb-uk.ac.uk				
CC	EMBL: X59714; CAA4234.1; -				
CC	ISSP: P19267; IRFM.				
CC	Malabar: 53482; -				
CC	InterPro: IPR000947; -				
CC	Plan: PF00808; CHFA_NFYB_HMP; 1.				
CC	PRINTS: PR00615; CCAATSUBUNITA.				
CC	PROSITE: PS00685; CHFA_NFYB; 1.				
CC	Transcription regulation: DNA-binding: Activator; Nuclear protein.				
FT	DOMAIN	1	29	A DOMAIN.	
FT	DOMAIN	30	115	B DOMAIN.	
FT	DOMAIN	120	179	C DOMAIN.	
FT	DOMAIN	36	42	BY SIMILARITY.	
FT	DNA BIND	179 AA	1895 MW	266213164546454 CDS64:	
SC	SEQUENCE	179 AA	1895 MW	266213164546454 CDS64:	

[illegible][illegible]















Thu Nov 29 08:24:21 2001

us-09-516-052-2\_copy\_28\_177.rsp

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UY 67 LWAM 70  
1:  
Ddb 62 KLA1 65

Search completed: November 28, 2001, 19:53:55  
Job time: 206 sec

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